SEQUENCE LISTING

(1) GENERAL INFORMATION:

    (i)   APPLICANT: SLIJKHUIS, HERMAN; SELTEN, GERARDUS CORNELIS MARIA; SMAAL, ERIC BASTIAAN

    (ii)   TITLE OF INVENTION: PROCESS FOR OXIDATION OF STEROIDS AND GENETICALLY ENGINEERED CELLS USED THEREIN

    (iii)   NUMBER OF SEQUENCES: 79

    (iv)   CORRESPONDENCE ADDRESS:
        (A)   ADDRESSEE: BIERMAN, MUSERLIAN & LUCAS
        (B)   STREET: 600 THIRD AVENUE
        (C)   CITY: NEW YORK
        (D)   STATE: NEW YORK
        (E)   COUNTRY: USA
        (F)   ZIP: 10016

    (v)   COMPUTER READABLE FORM:
        (A)   MEDIUM TYPE: FLOPPY DISK
        (B)   COMPUTER: IBM PC COMPATIBLE
        (C)   OPERATING SYSTEM: PC-DOS/MS-DOS
        (D)   SOFTWARE: MICROSOFT WORD 97

    (vi)   CURRENT APPLICATION DATA:
        (A)   APPLICATION NUMBER: 09/098,990
        (B)   FILING DATE: 17-JUN-1998

    (vii)   PRIOR APPLICATION DATA:
        (A)   APPLICATION NUMBER: 08/418,085
        (B)   FILING DATE: 06-APR-1995

    (vii)   PRIOR APPLICATION DATA:
        (A)   APPLICATION NUMBER: 08/054,185
        (B)   FILING DATE: 26-APR-1993

    (vii)   PRIOR APPLICATION DATA:
        (A)   APPLICATION NUMBER: 08/002,608
        (B)   FILING DATE: 11-JAN-1993

    (vii)   PRIOR APPLICATION DATA:

      (A) APPLICATION NUMBER: 07/474,857
      (B) FILING DATE: 30-OCT-1990

  (vii)   PRIOR APPLICATION DATA:
      (A) APPLICATION NUMBER: 07/474,798
      (B) FILING DATE: 16-JULY-1990

  (vii)   PRIOR APPLICATION DATA:
      (A) APPLICATION NUMBER: PCT/NL89/00072
      (B) FILING DATE: 25-SEPT-1989

  (vii)   PRIOR APPLICATION DATA:
      (A) APPLICATION NUMBER: NL88/200904.6
      (B) FILING DATE: 06-MAY-1988

  (vii)   PRIOR APPLICATION DATA:
      (A) APPLICATION NUMBER: NL/88/202080.3
      (B) FILING DATE: 03-SEP-1988

  (viii) ATTORNEY/AGENT INFORMATION:
      (A) NAME: CHARLES A. MUSERLIAN
      (B) REGISTRATION NUMBER: 19,683
      (C) REFERENCE/DOCKET NUMBER: 146.1169-
         CON-1-DIV-1

  (ix)   TELECOMMUNICATION INFORMATION:
      (A) TELEPHONE: (212) 661-8000
      (B) TELEFAX: (212) 661-8002

(2) INFORMATION FOR SEQ ID NO: 1:

  (i)   SEQUENCE CHARACTERISTICS:
      (A) LENGTH: 37 BASE PAIRS
      (B) TYPE: NUCLEIC ACID
      (C) STRANDEDNESS: SINGLE
      (D) TOPOLOGY: LINEAR

  (ix)   FEATURE:
      (D) OTHER INFORMATION: OLIGOMER SSC-1

  (xi)   SEQUENCE DESCRIPTION: SEQ ID NO: 1:

GGCTGACGAA GTCCTGAGAC ACTGGATTCA GCACTGG   37

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(2) INFORMATION FOR SEQ ID NO: 2:

    (i)   SEQUENCE CHARACTERISTICS:
            (A)   LENGTH: 177 BASE PAIRS
            (B)   TYPE: NUCLEIC ACID
            (C)   STRANDEDNESS: DOUBLE
            (D)   TOPOLOGY: LINEAR

    (ix)   FEATURE:
            (D)   OTHER INFORMATION: SYNTHETIC
                PSTI/HINDIII FRAGMENT

    (xi)   SEQUENCE DESCRIPTION: SEQ ID NO: 2:

```
TGCAGCAGCG GCGGCAATCA GTACTAAGAC CCCTAGGCCT            40

TACAGTGAGA TCCCCTCCCC TGGTGACAAT GGCTGGCTTA            80

ACCTCTACCA TTTCTGGAGG GAGAAGGGCT CACAGAGAAT           120

CCACTTTCGC CACATCGAGA ACTTCCAGAA GTATGGCCCC           160

ATTTACAGGG AGAAGCT                                    177
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(2) INFORMATION FOR SEQ ID NO: 3:

    (i)   SEQUENCE CHARACTERISTICS:
            (A)   LENGTH: 7336 BASE PAIRS
            (B)   TYPE: NUCLEIC ACID
            (C)   STRANDEDNESS: DOUBLE
            (D)   TOPOLOGY: UNKNOWN

    (ix)   FEATURE:
            (D)   OTHER INFORMATION: PLASMID pBHA-1

    (xi)   SEQUENCE DESCRIPTION: SEQ ID NO: 3:

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AATTCACCTC GAAAGCAAGC TGATAAACCG ATACAATTAA            40

AGGCTCCTTT TGGAGCCTTT TTTTTTGGAG ATTTTCAACG            80

TGAAAAAATT ATTATTCGCA ATTCCAAGCT AATTCACCTC           120
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GAAAGCAAGC TGATAAACCG ATACAATTAA AGGCTCCTTT                160

TGGAGCCTTT TTTTTTGGAG ATTTTCAACG TGAAAAAATT                200

ATTATTCGCA ATTCCAAGCT CTGCCTCGCG CGTTTCGGTG                240

ATGACGGTGA AAACCTCTGA CACATGCAGC TCCCGGAGAC                280

GGTCACAGCT TGTCTGTAAG CGGATGCAGA TCACGCGCCC                320

TGTAGCGGCG CATTAAGCGC GGCGGGTGTG GTGGTTACGC                360

GCAGCGTGAC CGCTACACTT GCCAGCGCCC TAGCGCCCGC                400

TCCTTTCGCT TTCTTCCCTT CCTTTCTCGC CACGTTCGCC                440

GGCTTTCCCC GTCAAGCTCT AAATCGGGGG CTCCCTTTAG                480

GGTTCCGATT TAGTGCTTTA CGGCACCTCG ACCCCAAAAA                520

ACTTGATTAG GGTGATGGTT CACGTAGTGG GCCATCGCCC                560

TGATAGACGG TTTTTCGCCC TTTGACGTTG GAGTCCACGT                600

TCTTTAATAG TGGACTCTTG TTCCAAACTG GAACAACACT                640

CAACCCTATC TCGGTCTATT CTTTTGATTT ATAAGGGATT                680

TTGCCGATTT CGGCCTATTG GTTAAAAAAT GAGCTGATTT                720

AACAAAAATT TAACGCGAAT TTTAACAAAA TATTAACGTT                760

TACAATTTGA TCTGCGCTCG GTCGTTCGGC TGCGGCGAGC                800

GGTATCAGCT CACTCAAAGG CGGTAATACG GTTATCCACA                840

GAATCAGGGG ATAACGCAGG AAAGAACATG TGAGCAAAAG                880

GCCAGCAAAA GGCCAGGAAC CGTAAAAAGG CCGCGTTGCT                920

GGCGTTTTTC CATAGGCTCC GCCCCCCTGA CGAGCATCAC                960

AAAAATCGAC GCTCAAGTCA GAGGTGGCGA AACCCGACAG               1000

GACTATAAAG ATACCAGGCG TTTCCCCCTG GAAGCTCCCT               1040
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CGTGCGCTCT CCTGTTCCGA CCCTGCCGCT TACCGGATAC   1080

CTGTCCGCCT TTCTCCCTTC GGGAAGCGTG GCGCTTTCTC   1120

ATAGCTCACG CTGTAGGTAT CTCAGTTCGG TGTAGGTCGT   1160

TCGCTCCAAG CTGGGCTGTG TGCACGAACC CCCCGTTCAG   1200

CCCGACCGCT GCGCCTTATC CGGTAACTAT CGTCTTGAGT   1240

CCAACCCGGT AAGACACGAC TTATCGCCAC TGGCAGCAGC   1280

CACTGGTAAC AGGATTAGCA GAGCGAGGTA TGTAGGCGGT   1320

GCTACAGAGT TCTTGAAGTG GTGGCCTAAC TACGGCTACA   1360

CTAGAAGGAC AGTATTTGGT ATCTGCGCTC TGCTGAAGCC   1400

AGTTACCTTC GGAAAAAGAG TTGGTAGCTC TTGATCCGGC   1440

AAACAAACCA CCGCTGGTAG CGGTGGTTTT TTTGTTTGCA   1480

AGCAGCAGAT TACGCGCAGA AAAAAGGAT CTCAAGAAGA   1520

TCCTTTGATC TTTTCTACGG GGTCTGACGC TCAGTGGAAC   1560

GAAAACTCAC GTTAAGGGAT TTTGGTCATG AGATTATCAA   1600

AAAGGATCTT CACCTAGATC CTTTTAAATT AAAAATGAAG   1640

TTTTAAATCA ATCTAAAGTA TATATGAGTA AACTTGGTCT   1680

GACAGTTACC AATGCTTAAT CAGTGAGGCA CCTATCTCAG   1720

CGATCTGTCT ATTTCGTTCA TCCATAGTTG CCTGACTCCC   1760

CGTCGTGTAG ATAACTACGA TACGGGAGGG CTTACCATCT   1800

GGCCCCAGTG CTGCAATGAT ACCGCGAGAC CCACGCTCAC   1840

CGGCTCCAGA TTTATCAGCA ATAAACCAGC CAGCCGGAAG   1880

GGCCGAGCGC AGAAGTGGTC CTGCAACTTT ATCCGCCTCC   1920

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ATCCAGTCTA TTAATTGTTG CCGGGAAGCT AGAGTAAGTA        1960

GTTCGCCAGT TAATAGTTTG CGCAACGTTG TTGCCATTGC        2000

TGCAGGCATC GTGGTGTCAC GCTCGTCGTT TGGTATGGCT        2040

TCATTCAGCT CCGGTTCCCA ACGATCAAGG CGAGTTACAT        2080

GATCCCCCAT GTTGTGCAAA AAAGCGGTTA GCTCCTTCGG        2120

TCCTCCGATC GTTGTCAGAA GTAAGTTGGC CGCAGTGTTA        2160

TCACTCATGG TTATGGCAGC ACTGCATAAT TCTCTTACTG        2200

TCATGCCATC CGTAAGATGC TTTTCTGTGA CTGGTGAGTA        2240

CTCAACCAAG TCATTCTGAG AATAGTGTAT GCGGCGACCG        2280

AGTTGCTCTT GCCCGGCGTC AACACGGGAT AATACCGCGC        2320

CACATAGCAG AACTTTAAAA GTGCTCATCA TTGGAAAACG        2360

TTCTTCGGGG CGAAAACTCT CAAGGATCTT ACCGCTGTTG        2400

AGATCCAGTT CGATGTAACC CACTCGTGCA CCCAACTGAT        2440

CTTCAGCATC TTTTACTTTC ACCAGCGTTT CTGGGTGAGC        2480

AAAAACAGGA AGGCAAAATG CCGCAAAAAA GGGAATAAGG        2520

GCGACACGGA AATGTTGAAT ACTCATACTC TTCCTTTTTC        2560

AATATTATTG AAGCAGACAG TTTTATTGTT CATGATGATA        2600

TATTTTTATC TTGTGCAATG TAACATCAGA GATTTTGAGA        2640

CACAACGTGG CTTTGTTGAA TAAATCGAAC TTTTGCTGAG        2680

TTGACTCCCC GCGCGCGATG GGTCGAATTT GCTTTCGAAA        2720

AAAAAGCCCG CTCATTAGGC GGGCTAAAAA AAAGCCCGCT        2760

CATTAGGCGG GCTCGAATTT CTGCCATTCA TCCGCTTATT        2800

ATCACTTATT CAGGCGTAGC AACCAGGCGT TTAAGGGCAC        2840
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CAATAACTGC CTTAAAAAAA TTACGCCCCG CCCTGCCACT          2880

CATCGCAGTA CTGTTGTAAT TCATTAAGCA TTCTGCCGAC          2920

ATGGAAGCCA TCACAGACGG CATGATGAAC CTGAATCGCC          2960

AGCGGCATCA GCACCTTGTC GCCTTGCGTA TAATATTTGC          3000

CCATAGTGAA AACGGGGGCG AAGAAGTTGT CCATATTCGC          3040

CACGTTTAAA TCAAAACTGG TGAAACTCAC CCAGGGATTG          3080

GCTGAGACGA AAAACATATT CTCAATAAAC CCTTTAGGGA          3120

AATAGGCCAG GTTTTCACCG TAACACGCCA CATCTTGCGA          3160

ATATATGTGT AGAAACTGCC GGAAATCGTC GTGGTATTCA          3200

CTCCAGAGCG ATGAAAACGT TTCAGTTTGC TCATGGAAAA          3240

CGGTGTAACA AGGGTGAACA CTATCCCATA TCACCAGCTC          3280

ACCGTCTTTC ATTGCCATAC GAAATTCCGG ATGAGCATTC          3320

ATCAGGCGGG CAAGAATGTG AATAAAGGCC GGATAAAACT          3360

TGTGCTTATT TTTCTTTACG GTCTTTAAAA AGGCCGTAAT          3400

ATCCAGCTAA ACGGTCTGGT TATAGGTACA TTGAGCAACT          3440

GACTGAAATG CCTCAAAATG TTCTTTACGA TGCCATTGGG          3480

ATATATCAAC GGTGGTATAT CCAGTGATTT TTTTCTCCAT          3520

TTTAGCTTCC TTAGCTCCTG AAAATCTCGA TAACTCAAAA          3560

AATACGCCCG GTAGTGATCT TATTTCATTA TGGTGAAAGT          3600

TGGAACCTCT TACGTGCCGA TCAACGTCTC ATTTTCGCCA          3640

AAAGTTGGCC CAGGGCTTCC CGGTATCAAC AGGGACACCA          3680

GGATTTATTT ATTCTGCGAA GTGATCTTCC GTCACAGGTA          3720
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TTTATTCGAA GACGAAAGGG CATCGCGCGC GGGGAATTCC   3760

CGGGAGAGCT CGATATCGCA TGCGGTACCT CTAGAAGAAG   3800

CTTGGAGACA AGGTAAAGGA TAAAACAGCA CAATTCCAAG   3840

AAAAACACGA TTTAGAACCT AAAAAGAACG AATTTGAACT   3880

AACTCATAAC CGAGAGGTAA AAAAAGAACG AAGTCGAGAT   3920

CAGGGAATGA GTTTATAAAA TAAAAAAAGC ACCTGAAAAG   3960

GTGTCTTTTT TTGATGGTTT TGAACTTGTT CTTTCTTATC   4000

TTGATACATA TAGAAATAAC GTCATTTTTA TTTTAGTTGC   4040

TGAAAGGTGC GTTGAAGTGT TGGTATGTAT GTGTTTTAAA   4080

GTATTGAAAA CCCTTAAAAT TGGTTGCACA GAAAAACCCC   4120

ATCTGTTAAA GTTATAAGTG ACTAAACAAA TAACTAAATA   4160

GATGGGGGTT TCTTTTAATA TTATGTGTCC TAATAGTAGC   4200

ATTTATTCAG ATGAAAAATC AAGGGTTTTA GTGGACAAGA   4240

CAAAAGTGG AAAAGTGAGA CCATGGAGAG AAAAGAAAAT   4280

CGCTAATGTT GATTACTTTG AACTTCTGCA TATTCTTGAA   4320

TTTAAAAAGG CTGAAAGAGT AAAAGATTGT GCTGAAATAT   4360

TAGAGTATAA ACAAAATCGT GAAACAGGCG AAAGAAAGTT   4400

GTATCGAGTG TGGTTTTGTA AATCCAGGCT TTGTCCAATG   4440

TGCAACTGGA GGAGAGCAAT GAAACATGGC ATTCAGTCAC   4480

AAAAGGTTGT TGCTGAAGTT ATTAAACAAA AGCCAACAGT   4520

TCGTTGGTTG TTTCTCACAT TAACAGTTAA AAATGTTTAT   4560

GATGGCGAAG AATTAAATAA GAGTTTGTCA GATATGGCTC   4600

AAGGATTTCG CCGAATGATG CAATATAAAA AAATTAATAA   4640

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AAATCTTGTT GGTTTTATGC GTGCAACGGA AGTGACAATA          4680

AATAATAAAG ATAATTCTTA TAATCAGCAC ATGCATGTAT          4720

TGGTATGTGT GGAACCAACT TATTTTAAGA ATACAGAAAA          4760

CTACGTGAAT CAAAAACAAT GGATTCAATT TTGGAAAAAG          4800

GCAATGAAAT TAGACTATGA TCCAAATGTA AAAGTTCAAA          4840

TGATTCGACC GAAAAATAAA TATAAATCGG ATATACAATC          4880

GGCAATTGAC GAAACTGCAA AATATCCTGT AAAGGATACG          4920

GATTTTATGA CCGATGATGA AGAAAGAAT TTGAAACGTT           4960

TGTCTGATTT GGAGGAAGGT TTACACCGTA AAAGGTTAAT          5000

CTCCTATGGT GGTTTGTTAA AAGAAATACA TAAAAAATTA          5040

AACCTTGATG ACACAGAAGA AGGCGATTTG ATTCATACAG          5080

ATGATGACGA AAAAGCCGAT GAAGATGGAT TTTCTATTAT          5120

TGCAATGTGG AATTGGGAAC GGAAAAATTA TTTTATTAAA          5160

GAGTAGTTCA ACAAACGGGC CAGTTTGTTG AAGATTAGAT          5200

GCTATAATTG TTATTAAAAG GATTGAAGGA TGCTTAGGAA          5240

GACGAGTTAT TAATAGCTGA ATAAGAACGG TGCTCTCCAA          5280

ATATTCTTAT TTAGAAAAGC AAATCTAAAA TTATCTGAAA          5320

AGGGAATGAG AATAGTGAAT GGACCAATAA TAATGACTAG          5360

AGAAGAAAGA ATGAAGATTG TTCATGAAAT TAAGGAACGA          5400

ATATTGGATA AATATGGGGA TGATGTTAAG GCTATTGGTG          5440

TTTATGGCTC TCTTGGTCGT CAGACTGATG GGCCCTATTC .        5480

GGATATTGAG ATGATGTGTG TCATGTCAAC AGAGGAAGCA          5520
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GAGTTCAGCC  ATGAATGGAC  AACCGGTGAG  TGGAAGGTGG          5560

AAGTGAATTT  TGATAGCGAA  GAGATTCTAC  TAGATTATGC          5600

ATCTCAGGTG  GAATCAGATT  GGCCGCTTAC  ACATGGTCAA          5640

TTTTTCTCTA  TTTTGCCGAT  TTATGATTCA  GGTGGATACT          5680

TAGAGAAAGT  GTATCAAACT  GCTAAATCGG  TAGAAGCCCA          5720

AACGTTCCAC  GATGCGATTT  GTGCCCTTAT  CGTAGAAGAG          5760

CTGTTTGAAT  ATGCAGGCAA  ATGGCGTAAT  ATTCGTGTGC          5800

AAGGACCGAC  AACATTTCTA  CCATCCTTGA  CTGTACAGGT          5840

AGCAATGGCA  GGTGCCATGT  TGATTGGTCT  GCATCATCGC          5880

ATCTGTTATA  CGACGAGCGC  TTCGGTCTTA  ACTGAAGCAG          5920

TTAAGCAATC  AGATCTTCCT  TCAGGTTATG  ACCATCTGTG          5960

CCAGTTCGTA  ATGTCTGGTC  AACTTTCCGA  CTCTGAGAAA          6000

CTTCTGGAAT  CGCTAGAGAA  TTTCTGGAAT  GGGATTCAGG          6040

AGTGGACAGA  ACGACACGGA  TATATAGTGG  ATGTGTCAAA          6080

ACGCATACCA  TTTTGAACGA  TGACCTCTAA  TAATTGTTAA          6120

TCATGTTGGT  TACGTATTTA  TTAACTTCTC. CTAGTATTAG          6160

TAATTATCAT  GGCTGTCATG  GCGCATTAAC  GGAATAAAGG          6200

GTGTGCTTAA  ATCGGGCCAT  TTTGCGTAAT  AAGAAAAAGG          6240

ATTAATTATG  AGCGAATTGA  ATTAATAATA  AGGTAATAGA          6280

TTTACATTAG  AAAATGAAAG  GGGATTTTAT  GCGTGAGAAT          6320

GTTACAGTCT  ATCCCGGCAT  TGCCAGTCGG  GGATATTAAA          6360

AAGAGTATAG  GTTTTTATTG  CGATAAACTA  GGTTTCACTT          6400

TGGTTCACCA  TGAAGATGGA  TTCGCAGTTC  TAATGTGTAA          6440
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TGAGGTTCGG ATTCATCTAT GGGAGGCAAG TGATGAAGGC          6480

TGGCGCTCTC GTAGTAATGA TTCACCGGTT TGTACAGGTG          6520

CGGAGTCGTT TATTGCTGGT ACTGCTAGTT GCCGCATTGA          6560

AGTAGAGGGA ATTGATGAAT TATATCAACA TATTAAGCCT          6600

TTGGGCATTT TGCACCCCAA TACATCATTA AAAGATCAGT          6640

GGTGGGATGA ACGAGACTTT GCAGTAATTG ATCCCGACAA          6680

CAATTTGATT AGCTTTTTTC AACAAATAAA AAGCTAAAAT          6720

CTATTATTAA TCTGTTCAGC AATCGGGCGC GATTGCTGAA          6760

TAAAAGATAC GAGAGACCTC TCTTGTATCT TTTTTATTTT          6800

GAGTGGTTTT GTCCGTTACA CTAGAAAACC GAAAGACAAT          6840

AAAAATTTTA TTCTTGCTGA GTCTGGCTTT CGGTAAGCTA          6880

GACAAAACGG ACAAAATAAA AATTGGCAAG GGTTTAAAGG          6920

TGGAGATTTT TTGAGTGATC TTCTCAAAAA ATACTACCTG          6960

TCCCTTGCTG ATTTTTAAAC GAGCACGAGA GCAAAACCCC          7000

CCTTTGCTGA GGTGGCAGAG GGCAGGTTTT TTTGTTTCTT          7040

TTTTCTCGTA AAAAAAGAA AGGTCTTAAA GGTTTTATGG          7080

TTTTGGTCGG CACTGCCGAC AGCCTCGCAG GACACACACT          7120

TTATGAATAT AAAGTATAGT GTGTTATACT TTACTTGGAA          7160

GTGGTTGCCG GAAAGAGCGA AAATGCCTCA CATTTGTGCC          7200

ACCTAAAAAG GAGCGATTTA CATATGAGTT ATGCAGTTTG          7240

TAGAATGCAA AAAGTGAAAT CAGGGGGATC CTCTAGAGTC          7280

GAGCTCAAGC TAGCTTGGTA CGTACCAGAT CTGAGATCAC          7320
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GCGTTCTAGA GGTCGA   7336

(2)   INFORMATION FOR SEQ ID NO: 4:

       (i)   SEQUENCE CHARACTERISTICS:
                   (A)   LENGTH: 27 BASE PAIRS
                   (B)   TYPE: NUCLEIC ACID
                   (C)   STRANDEDNESS: DOUBLE
                   (D)   TOPOLOGY: UNKNOWN

       (ix)   FEATURE:
                   (D)   OTHER INFORMATION: SPHI/STUI FRAGMENT
                          IN pGBSCC-4

       (xi)   SEQUENCE DESCRIPTION: SEQ ID NO: 4:

CATATGATCA GTACTAAGAC CCCTAGG   27

(2)   INFORMATION FOR SEQ ID NO: 5:

       (i)   SEQUENCE CHARACTERISTICS:
                   (A)   LENGTH: 31 BASE PAIRS
                   (B)   TYPE: NUCLEIC ACID
                   (C)   STRANDEDNESS: DOUBLE
                   (D)   TOPOLOGY: UNKNOWN

       (ix)   FEATURE:
                   (D)   OTHER INFORMATION: SPHI/STUI FRAGMENT
                          IN pGBSCC-4

       (xi)   SEQUENCE DESCRIPTION: SEQ ID NO: 5:

CCTAGGGGTC TTAGTACTGA TCATATGCAT G   31

(2)   INFORMATION FOR SEQ ID NO: 6:

       (i)   SEQUENCE CHARACTERISTICS:
                   (A)   LENGTH: 41 BASE PAIRS
                   (B)   TYPE: NUCLEIC ACID
                   (C)   STRANDEDNESS: DOUBLE
                   (D)   TOPOLOGY: UNKNOWN

(ix)   FEATURE:
            (D)   OTHER INFORMATION: SPHI/STUI FRAGMENT
                  IN pGBSSC-3, FIGURE 7

(xi)   SEQUENCE DESCRIPTION: SEQ ID NO: 6:

CTGCAGCAGC GGCGGCAATC AGTACTAAGA CCCCTAGGCC T   41

(2)   INFORMATION FOR SEQ ID NO: 7:

(i)   SEQUENCE CHARACTERISTICS:
            (A)   LENGTH: 24 BASE PAIRS
            (B)   TYPE: NUCLEIC ACID
            (C)   STRANDEDNESS: SINGLE
            (D)   TOPOLOGY: LINEAR

(ix)   FEATURE:
            (D)   OTHER INFORMATION: NDEI RESTRICTION
                  SITE AT THE ATG INITIATION CODON OF
                  THE LACZ GENE IN PTZ18R

(xi)   SEQUENCE DESCRIPTION: SEQ ID NO: 7:

CAGGAAACAC ATATGACCAT GATT   24

(2)   INFORMATION FOR SEQ ID NO: 8:

(i)   SEQUENCE CHARACTERISTICS:
            (A)   LENGTH: 108 BASE PAIRS
            (B)   TYPE: NUCLEIC ACID
            (C)   STRANDEDNESS: DOUBLE
            (D)   TOPOLOGY: UNKNOWN

(ix)   FEATURE:
            (D)   OTHER INFORMATION: LACTASE TERMINATOR

(xi)   SEQUENCE DESCRIPTION: SEQ ID NO: 8:

TCGACGCGGC CGCAGATCTG ATATCTCGAG AATTTATACT   40

TAGATAAGTA TGTACTTACA GGTATATTTC TATGAGATAC   80

TGATGTATAC ATGCATGATA ATATTTAA   108

(2)   INFORMATION FOR SEQ ID NO: 9:

    (i)   SEQUENCE CHARACTERISTICS:
           (A)   LENGTH: 44 BASE PAIRS
           (B)   TYPE: NUCLEIC ACID
           (C)   STRANDEDNESS: DOUBLE
           (D)   TOPOLOGY: UNKNOWN

    (ix)   FEATURE:
           (D)   OTHER INFORMATION: SALI/XHOI FRAGMENT
               IN pGBSCC-6

    (xi)   SEQUENCE DESCRIPTION: SEQ ID NO: 9:

TCGACAAAAA TGATCAGTAC TAAGACTCCT AGGCCTATCG ATTC   44

(2)   INFORMATION FOR SEQ ID NO: 10:

    (i)   SEQUENCE CHARACTERISTICS:
           (A)   LENGTH: 44 BASE PAIRS
           (B)   TYPE: NUCLEIC ACID
           (C)   STRANDEDNESS: DOUBLE
           (D)   TOPOLOGY: UNKNOWN

    (ix)   FEATURE:
           (D)   OTHER INFORMATION: SALI/XHOI FRAGMENT
               IN pGBSCC-6

    (xi)   SEQUENCE DESCRIPTION: SEQ ID NO: 10:

TCGAGAATCG ATAGGCCTAG GAGTCTTAGT ACTGATCATT TTTG   44

(2)   INFORMATION FOR SEQ ID NO: 11:

    (i)   SEQUENCE CHARACTERISTICS:
           (A)   LENGTH: 158 BASE PAIRS
           (B)   TYPE: NUCLEIC ACID
           (C)   STRANDEDNESS: DOUBLE
           (D)   TOPOLOGY: UNKNOWN

    (ix)   FEATURE:

(D)   OTHER INFORMATION: SALI/XHOI
        SYNTHETIC DNA IN PLASMID pGBSCC-11

(xi)   SEQUENCE DESCRIPTION: SEQ ID NO: 11:

TCGACAAAAA TGTTGGCTCG AGGTTTGCCA TTGAGATCCG   40

CTTTGGTTAA GGCTTGTCCA CCAATCTTGT CCACTGTTGG   80

TGAAGGTTGG GGTCACCACA GAGTTGGTAC TGGTGAAGGT   120

GCTGGTATCA GTACTAAGAC TCCTAGGCCT ATCGATTC   158

(2)   INFORMATION FOR SEQ ID NO: 12:

        (i)   SEQUENCE CHARACTERISTICS:
                   (A)   LENGTH: 158 BASE PAIRS
                   (B)   TYPE: NUCLEIC ACID
                   (C)   STRANDEDNESS: DOUBLE
                   (D)   TOPOLOGY: UNKNOWN

        (ix)   FEATURE:
                   (D)   OTHER INFORMATION: SALI/XHOI
                         SYNTHETIC DNA IN PLASMID pGBSCC-11

        (xi)   SEQUENCE DESCRIPTION: SEQ ID NO: 12:

TCGAGAATCG ATAGGCCTAG GAGTCTTAGT ACTGATACCA   40

GCACCTTCAC CAGTACCAAC TCTGTGGTGA CCCCAACCTT   80

CACCAACAGT GGACAAGATT GGTGGACAAG CCTTAACCAA   120

AGCGGATCTC AATGGCAAAC CTCGAGCCAA CATTTTTG   158

(2)   INFORMATION FOR SEQ ID NO: 13:

        (i)   SEQUENCE CHARACTERISTICS:
                   (A)   LENGTH: 161 BASE PAIRS
                   (B)   TYPE: NUCLEIC ACID
                   (C)   STRANDEDNESS: DOUBLE
                   (D)   TOPOLOGY: UNKNOWN

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(ix)   FEATURE:
             (D)   OTHER INFORMATION: SALI/XHOI
                   SYNTHETIC DNA IN pGBSSC-14

(xi)   SEQUENCE DESCRIPTION: SEQ ID NO: 13:

TCGACAAAAA TGTTGTCTCG AGCTATCTTC AGAAACCCAG   40

TTATCAACAG AACTTTGTTG AGAGCTAGAC CAGGTGCTTA   80

CCACGCTACT AGATTGACTA AGAACACTTT CATCCAATCC   120

AGAAAGTACA TCAGTACTAA GACTCCTAGG CCTATCGATT   160

C   161

(2) INFORMATION FOR SEQ ID NO: 14:

     (i)   SEQUENCE CHARACTERISTICS:
                 (A)   LENGTH: 161 BASE PAIRS
                 (B)   TYPE: NUCLEIC ACID
                 (C)   STRANDEDNESS: DOUBLE
                 (D)   TOPOLOGY: UNKNOWN

     (ix)   FEATURE:
                 (D)   OTHER INFORMATION: SALI/XHOI
                       SYNTHETIC DNA IN pGBSCC-14

     (xi)   SEQUENCE DESCRIPTION: SEQ ID NO: 14:

TCGAGAATCG ATAGGCCTAG GAGTCTTAGT ACTGATGTAC   40

TTTCTGGATT GGATGAAAGT GTTCTTAGTC AATCTAGTAG   80

CGTGGTAAGC ACCTGCTCTA GCTCTCAACA AAGTTCTGTT   120

GATAACTGGG TTTCTGAAGA TAGCTCGAGA CAACATTTTT   160

G   161

(2) INFORMATION FOR SEQ ID NO: 15:

     (i)   SEQUENCE CHARACTERISTICS:

        (A)   LENGTH: 30 BASE PAIRS
        (B)   TYPE: NUCLEIC ACID
        (C)   STRANDEDNESS: DOUBLE
        (D)   TOPOLOGY: LINEAR

  (ix)   FEATURE:
        (D)   OTHER INFORMATION: OLIGOMER 17
             ALPHA-1

  (xi)   SEQUENCE DESCRIPTION: SEQ ID NO: 15:

AGTGGCCACT TTGGGACGCC CAGAGAATTC   30

(2)   INFORMATION FOR SEQ ID NO: 16:

  (i)   SEQUENCE CHARACTERISTICS:
        (A)   LENGTH: 36 BASE PAIRS
        (B)   TYPE: NUCLEIC ACID
        (C)   STRANDEDNESS: DOUBLE
        (D)   TOPOLOGY: LINEAR

  (ix)   FEATURE:
        (D)   OTHER INFORMATION: OLIGOMER 17
             ALPHA-2

  (xi)   SEQUENCE DESCRIPTION: SEQ ID NO: 16:

GAGGCTCCTG GGGTACTTGG CACCAGAGTG CTTGGT   36

(2)   INFORMATION FOR SEQ ID NO: 17:

  (i)   SEQUENCE CHARACTERISTICS:
        (A)   LENGTH: 43 BASE PAIRS
        (B)   TYPE: NUCLEIC ACID
        (C)   STRANDEDNESS: SINGLE
        (D)   TOPOLOGY: LINEAR

  (ix)   FEATURE:
        (D)   OTHER INFORMATION: SEQUENCE OF pGB17
             ALPHA-3 MUTATED BY SITE DIRECTED
             MUTAGENESIS, FIGURE 23

  (xi)   SEQUENCE DESCRIPTION: SEQ ID NO: 17:

TCTTTGTCCT GACTGCTGCC ACCCAGACAC AATGTGGCTG CTC   43

(2)   INFORMATION FOR SEQ ID NO: 18:

    (i)   SEQUENCE CHARACTERISTICS:
          (A)   LENGTH: 43 BASE PAIRS
          (B)   TYPE: NUCLEIC ACID
          (C)   STRANDEDNESS: SINGLE
          (D)   TOPOLOGY: LINEAR

    (ix)   FEATURE:
          (D)   OTHER INFORMATION: SYNTHETIC OLIGOMER
              17 ALPHA-3 WITH SALI SITE

    (xi)   SEQUENCE DESCRIPTION: SEQ ID NO: 18:

TCTTTGTCCT GACTGCTGCC AGTCGACAAA AATGTGGCTG CTC   43

(2)   INFORMATION FOR SEQ ID NO: 19:

    (i)   SEQUENCE CHARACTERISTICS:
          (A)   LENGTH: 31 BASE PAIRS
          (B)   TYPE: NUCLEIC ACID
          (C)   STRANDEDNESS: DOUBLE
          (D)   TOPOLOGY: LINEAR

    (ix)   FEATURE:
          (D)   OTHER INFORMATION: SEQUENCE OF pGB17
              ALPHA-3 MUTATED BY SITE DIRECTED
              MUTAGENESIS TO CREATE A NDEI SITE,
              FIGURE 25

    (xi)   SEQUENCE DESCRIPTION: SEQ ID NO: 19:

GCTGCCACCC AGACACAATG TGGCTGCTCC T   31

(2)   INFORMATION FOR SEQ ID NO: 20:

    (i)   SEQUENCE CHARACTERISTICS:
          (A)   LENGTH: 31 BASE PAIRS
          (B)   TYPE: NUCLEIC ACID

```
                (C)   STRANDEDNESS:  DOUBLE
                (D)   TOPOLOGY:  LINEAR

        (ix)  ·     FEATURE:
                (D)   OTHER INFORMATION:  SYNTHETIC OLIGOMER
                      17 ALPHA-4


        (xi)        SEQUENCE DESCRIPTION: SEQ ID NO: 20:

GCTGCCACCC AGACCATATG TGGCTGCTCC T                              31


(2)     INFORMATION FOR SEQ ID NO: 21:

        (i)         SEQUENCE CHARACTERISTICS:
                (A)   LENGTH:  ·30 BASE PAIRS
                (B)   TYPE:  NUCLEIC ACID
                (C)   STRANDEDNESS:  SINGLE
                (D)   TOPOLOGY:  LINEAR

        (ix)        FEATURE:
                (D)   OTHER INFORMATION:  OLIGOMER C21-1

        (xi)        SEQUENCE DESCRIPTION: SEQ ID NO: 21:

GATGATGCTG CAGGTAAGCA GAGAGAATTC                                30


(2)     INFORMATION FOR SEQ ID NO: 22:

        (i)         SEQUENCE CHARACTERISTICS:
                (A)   LENGTH:  15 BASE PAIRS
                (B)   TYPE:  NUCLEIC ACID
                (C)   STRANDEDNESS:  SINGLE
                (D)   TOPOLOGY:  LINEAR

        (ix)        FEATURE:
                (D)   OTHER INFORMATION:  OLIGOMER C21-2

        (xi)        SEQUENCE DESCRIPTION: SEQ ID NO: 22:

AAGCAGAGAG AATTC                                                15
```

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(2)   INFORMATION FOR SEQ ID NO: 23:

    (i)   SEQUENCE CHARACTERISTICS:
        (A)   LENGTH: 36 BASE PAIRS
        (B)   TYPE: NUCLEIC ACID
        (C)   STRANDEDNESS: SINGLE
        (D)   TOPOLOGY: LINEAR

    (ix)   FEATURE:
        (D)   OTHER INFORMATION: OLIGOMER C21-3

    (xi)   SEQUENCE DESCRIPTION: SEQ ID NO: 23:

CTTCCACCGG CCCGATAGCA GGTGAGCGCC ACTGAG   36

(2)   INFORMATION FOR SEQ ID NO: 24:

    (i)   SEQUENCE CHARACTERISTICS:
        (A)   LENGTH: 36 BASE PAIRS
        (B)   TYPE: NUCLEIC ACID
        (C)   STRANDEDNESS: SINGLE
        (D)   TOPOLOGY: LINEAR

    (ix)   FEATURE:
        (D)   OTHER INFORMATION: OLIGOMER C21-4

    (xi)   SEQUENCE DESCRIPTION: SEQ ID NO: 24:

CTCACTGATA TCCATATGGT CCTCGCAGGG CTGCTG   36

(2)   INFORMATION FOR SEQ ID NO: 25:

    (i)   SEQUENCE CHARACTERISTICS:
        (A)   LENGTH: 27 BASE PAIRS
        (B)   TYPE: NUCLEIC ACID
        (C)   STRANDEDNESS: SINGLE
        (D)   TOPOLOGY: LINEAR

    (ix)   FEATURE:
        (D)   OTHER INFORMATION: OLIGOMER C21-5

    (xi)   SEQUENCE DESCRIPTION: SEQ ID NO: 25:

AGCTCAGAAT TCCTTCTGGA TGGTCAC   27

(2)   INFORMATION FOR SEQ ID NO: 26:

       (i)   SEQUENCE CHARACTERISTICS:
                   (A)   LENGTH: 12 BASE PAIRS
                   (B)   TYPE: NUCLEIC ACID
                   (C)   STRANDEDNESS: DOUBLE
                   (D)   TOPOLOGY: UNKNOWN

       (ix)   FEATURE:
                   (D)   OTHER INFORMATION: FIGURE 29,
                         pGBC21-2

       (xi)   SEQUENCE DESCRIPTION: SEQ ID NO: 26:

CCAGCCATGG TC   12

(2)   INFORMATION FOR SEQ ID NO: 27:

       (i)   SEQUENCE CHARACTERISTICS:
                   (A)   LENGTH: 9 BASE PAIRS
                   (B)   TYPE: NUCLEIC ACID
                   (C)   STRANDEDNESS: DOUBLE
                   (D)   TOPOLOGY: UNKNOWN

       (ix)   FEATURE:
                   (D)   OTHER INFORMATION: FIGURE 29,
                         pGBC21-2

       (xi)   SEQUENCE DESCRIPTION: SEQ ID NO: 27:

AAGGAATTC   9

(2)   INFORMATION FOR SEQ ID NO: 28:

       (i)   SEQUENCE CHARACTERISTICS:
                   (A)   LENGTH: 21 BASE PAIRS
                   (B)   TYPE: NUCLEIC ACID
                   (C)   STRANDEDNESS: SINGLE
                   (D)   TOPOLOGY: LINEAR

(ix)   FEATURE:
             (D)   OTHER INFORMATION: OLIGOMER C21-4

(xi)   SEQUENCE DESCRIPTION: SEQ ID NO: 28:

CTCACTGATA TCCATATGGT C   21

(2)   INFORMATION FOR SEQ ID NO: 29:

     (i)   SEQUENCE CHARACTERISTICS:
            (A)   LENGTH: 15 BASE PAIRS
            (B)   TYPE: NUCLEIC ACID
            (C)   STRANDEDNESS: SINGLE
            (D)   TOPOLOGY: LINEAR

     (ix)   FEATURE:
            (D)   OTHER INFORMATION: OLIGOMER C21-5

     (xi)   SEQUENCE DESCRIPTION: SEQ ID NO: 29:

AAGGAATTCT GAGCT   15

(2)   INFORMATION FOR SEQ ID NO: 30:

     (i)   SEQUENCE CHARACTERISTICS:
            (A)   LENGTH: 36 BASE PAIRS
            (B)   TYPE: NUCLEIC ACID
            (C)   STRANDEDNESS: SINGLE
            (D)   TOPOLOGY: LINEAR

     (ix)   FEATURE:
            (D)   OTHER INFORMATION: OLIGOMER C21-6

     (xi)   SEQUENCE DESCRIPTION: SEQ ID NO: 30:

CCTCTGCCTG GGTCGACAAA AATGGTCCTC GCAGGG   36

(2)   INFORMATION FOR SEQ ID NO: 31:

     (i)   SEQUENCE CHARACTERISTICS:
            (A)   LENGTH: 36 BASE PAIRS

```
            (B)   TYPE:  NUCLEIC ACID
            (C)   STRANDEDNESS:  DOUBLE
            (D)   TOPOLOGY:  UNKNOWN

    (ix)    FEATURE:
            (D)   OTHER INFORMATION:  PGBC21-2,
                  FIGURE 33

    (xi)    SEQUENCE DESCRIPTION: SEQ ID NO: 31:

CCTCTGCCTG GGTCTCCAGC CATGGTCCTC GCAGGG                    36


(2)   INFORMATION FOR SEQ ID NO: 32:

    (i)     SEQUENCE CHARACTERISTICS:
            (A)   LENGTH:  18 BASE PAIRS
            (B)   TYPE:  NUCLEIC ACID
            (C)   STRANDEDNESS:  SINGLE
            (D)   TOPOLOGY:  LINEAR

    (ix)    FEATURE:
            (D)   OTHER INFORMATION:  OLIGOMER 11 BETA-1

    (xi)    SEQUENCE DESCRIPTION: SEQ ID NO: 32:

GGCAGTGTGC TGACACGA                                        18


(2)   INFORMATION FOR SEQ ID NO: 33:

    (i)     SEQUENCE CHARACTERISTICS:
            (A)   LENGTH:  30 BASE PAIRS
            (B)   TYPE:  NUCLEIC ACID
            (C)   STRANDEDNESS:  SINGLE
            (D)   TOPOLOGY:  LINEAR

    (ix)    FEATURE:
            (D)   OTHER INFORMATION:  OLIGOMER 11 BETA-2

    (xi)    SEQUENCE DESCRIPTION: SEQ ID NO: 33:

CCGCACCCTG GCCTTTGCCC ACAGTGCCAT                           30
```

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(2)   INFORMATION FOR SEQ ID NO: 34:

    (i)   SEQUENCE CHARACTERISTICS:
                (A)   LENGTH: 36 BASE PAIRS
                (B)   TYPE: NUCLEIC ACID
                (C)   STRANDEDNESS: SINGLE
                (D)   TOPOLOGY: LINEAR

    (ix)   FEATURE:
                (D)   OTHER INFORMATION: OLIGOMER 11 BETA-3

    (xi)   SEQUENCE DESCRIPTION: SEQ ID NO: 34:

CAGCTCAAAG AGAGTCATCA GCAAGGGGAA GGCTGT   36

(2)   INFORMATION FOR SEQ ID NO: 35:

    (i)   SEQUENCE CHARACTERISTICS:
                (A)   LENGTH: 42 BASE PAIRS
                (B)   TYPE: NUCLEIC ACID
                (C)   STRANDEDNESS: SINGLE
                (D)   TOPOLOGY: LINEAR

    (ix)   FEATURE:
                (D)   OTHER INFORMATION: OLIGOMER 11 BETA-4

    (xi)   SEQUENCE DESCRIPTION: SEQ ID NO: 35:

TTTGATATCG AATTCCATAT GGGCACCAGA GGTGCTGCAG CC   42

(2)   INFORMATION FOR SEQ ID NO: 36:

    (i)   SEQUENCE CHARACTERISTICS:
                (A)   LENGTH: 42 BASE PAIRS
                (B)   TYPE: NUCLEIC ACID
                (C)   STRANDEDNESS: SINGLE
                (D)   TOPOLOGY: LINEAR

    (ix)   FEATURE:
                (D)   OTHER INFORMATION: OLIGOMER 11 BETA-5

    (xi)   SEQUENCE DESCRIPTION: SEQ ID NO: 36:

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TAACGATATC CTCGAGGGTA CCTACTGGAT GGCCCGGAAG GT   42

(2) INFORMATION FOR SEQ ID NO: 37:

   (i)   SEQUENCE CHARACTERISTICS:
       (A) LENGTH: 39 BASE PAIRS
       (B) TYPE: NUCLEIC ACID
       (C) STRANDEDNESS: SINGLE
       (D) TOPOLOGY: LINEAR

   (ix) FEATURE:
       (D) OTHER INFORMATION: OLIGOMER 11 BETA-6

   (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 37:

CTTCAGTCGA CAAAAATGGG CACCAGAGGT GCTGCAGCC   39

(2) INFORMATION FOR SEQ ID NO: 38:

   (i)   SEQUENCE CHARACTERISTICS:
       (A) LENGTH: 18 BASE PAIRS
       (B) TYPE: NUCLEIC ACID
       (C) STRANDEDNESS: DOUBLE
       (D) TOPOLOGY: UNKNOWN

   (ix) FEATURE:
       (D) OTHER INFORMATION: REGION IN 11 BETA
         cDNA HOMOLOGOUS TO PRIMERS, FIGURE 36

   (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 38:

CGCCTACTGG GCACCAGA   18

(2) INFORMATION FOR SEQ ID NO: 39:

   (i)   SEQUENCE CHARACTERISTICS:
       (A) LENGTH: 21 BASE PAIRS
       (B) TYPE: NUCLEIC ACID
       (C) STRANDEDNESS: DOUBLE
       (D) TOPOLOGY: UNKNOWN

(ix)   FEATURE:
            (D)   OTHER INFORMATION: REGION IN 11 BETA
                  cDNA HOMOLOGOUS TO PRIMERS, FIGURE 36

(xi)   SEQUENCE DESCRIPTION: SEQ ID NO: 39:

GCCATCCAGT AGTCGTGTCA G   21

(2)   INFORMATION FOR SEQ ID NO: 40:

     (i)   SEQUENCE CHARACTERISTICS:
                (A)   LENGTH: 30 BASE PAIRS
                (B)   TYPE: NUCLEIC ACID
                (C)   STRANDEDNESS: SINGLE
                (D)   TOPOLOGY: LINEAR

     (ix)   FEATURE:
                (D)   OTHER INFORMATION: OLIGOMER 11 BETA-4,
                      FIGURE 36

     (xi)   SEQUENCE DESCRIPTION: SEQ ID NO: 40:

TTTGATATCG AATTCCATAT GGGCACCAGA   30

(2)   INFORMATION FOR SEQ ID NO: 41:

     (i)   SEQUENCE CHARACTERISTICS:
                (A)   LENGTH: 33 BASE PAIRS
                (B)   TYPE: NUCLEIC ACID
                (C)   STRANDEDNESS: SINGLE
                (D)   TOPOLOGY: LINEAR

     (ix)   FEATURE:
                (D)   OTHER INFORMATION: OLIGOMER 11 BETA-5,
                      FIGURE 36

     (xi)   SEQUENCE DESCRIPTION: SEQ ID NO: 41:

GCCATCCAGT AGGTACCCTC GAGGATATCG TTA   33

(2)   INFORMATION FOR SEQ ID NO: 42:

422161_1

(i)   SEQUENCE CHARACTERISTICS:
        (A)   LENGTH: 27 BASE PAIRS
        (B)   TYPE: NUCLEIC ACID
        (C)   STRANDEDNESS: SINGLE
        (D)   TOPOLOGY: UNKNOWN

(ix)   FEATURE:
        (D)   OTHER INFORMATION: OLIGOMER 11 BETA-6,
            FIGURE 37

(xi)   SEQUENCE DESCRIPTION: SEQ ID NO: 42:

CTTCAGTCGA CAAAAATGGG CACCAGA   27

(2)   INFORMATION FOR SEQ ID NO: 43:

     (i)   SEQUENCE CHARACTERISTICS:
           (A)   LENGTH: 39 BASE PAIRS
           (B)   TYPE: NUCLEIC ACID
           (C)   STRANDEDNESS: SINGLE
           (D)   TOPOLOGY: LINEAR

    (ix)   FEATURE:
           (D)   OTHER INFORMATION: OLIGOMER ADX-1

    (xi)   SEQUENCE DESCRIPTION: SEQ ID NO: 43:

CTTCAGTCGA CAAAAATGAG CAGCTCAGAA GATAAAATA   39

(2)   INFORMATION FOR SEQ ID NO: 44:

     (i)   SEQUENCE CHARACTERISTICS:
           (A)   LENGTH: 40 BASE PAIRS
           (B)   TYPE: NUCLEIC ACID
           (C)   STRANDEDNESS: SINGLE
           (D)   TOPOLOGY: LINEAR

    (ix)   FEATURE:
           (D)   OTHER INFORMATION: OLIGOMER ADX-2

    (xi)   SEQUENCE DESCRIPTION: SEQ ID NO: 44:

TGTAAGGTAC CCGGGATCCT TATTCTATCT TTGAGGAGTT   40

(2)   INFORMATION FOR SEQ ID NO: 45:

    (i)   SEQUENCE CHARACTERISTICS:
            (A)   LENGTH: 18 BASE PAIRS
            (B)   TYPE: NUCLEIC ACID
            (C)   STRANDEDNESS: DOUBLE
            (D)   TOPOLOGY: UNKNOWN

    (ix)   FEATURE:
            (D)   OTHER INFORMATION: REGION OF ADX
                 mRNA/cDNA HOMOLOGOUS TO THE PRIMERS,
                 FIGURE 38

    (xi)   SEQUENCE DESCRIPTION: SEQ ID NO: 45:

CGAGCGCAGA GCAGCTCA   18

(2)   INFORMATION FOR SEQ ID NO: 46:

    (i)   SEQUENCE CHARACTERISTICS:
            (A)   LENGTH: 18 BASE PAIRS
            (B)   TYPE: NUCLEIC ACID
            (C)   STRANDEDNESS: DOUBLE
            (D)   TOPOLOGY: UNKNOWN

    (ix)   FEATURE:
            (D)   OTHER INFORMATION: REGION OF ADX
                 mRNA/cDNA HOMOLOGOUS TO THE PRIMERS,
                 FIGURE 38

    (xi)   SEQUENCE DESCRIPTION: SEQ ID NO: 46:

ATAGAATAAA TAGGAATA   18

(2)   INFORMATION FOR SEQ ID NO: 47:

    (i)   SEQUENCE CHARACTERISTICS:
            (A)   LENGTH: 27 BASE PAIRS
            (B)   TYPE: NUCLEIC ACID
            (C)   STRANDEDNESS: SINGLE
            (D)   TOPOLOGY: LINEAR

```
(ix)        FEATURE:
            (D)   OTHER INFORMATION:   OLIGOMER ADX-1,
                  FIGURE 38

(xi)        SEQUENCE DESCRIPTION: SEQ ID NO: 47:

CTTCAGTCGA CAAAAATGAG CAGCTCA                                    27


(2)   INFORMATION FOR SEQ ID NO: 48:

      (i)        SEQUENCE CHARACTERISTICS:
                 (A)   LENGTH:  28 BASE PAIRS
                 (B)   TYPE:  NUCLEIC ACID
                 (C)   STRANDEDNESS:  SINGLE
                 (D)   TOPOLOGY:  LINEAR

      (ix)       FEATURE:
                 (D)   OTHER INFORMATION:  OLIGOMER ADX-2,
                       FIGURE 38

      (xi)       SEQUENCE DESCRIPTION: SEQ ID NO: 48:

ATAGAATAAG GATCCCGGGT ACCTTACA                                   28


(2)   INFORMATION FOR SEQ ID NO: 49:

      (i)        SEQUENCE CHARACTERISTICS:
                 (A)   LENGTH:  15 BASE PAIRS
                 (B)   TYPE:  NUCLEIC ACID
                 (C)   STRANDEDNESS:  SINGLE
                 (D)   TOPOLOGY:  LINEAR

      (ix)       FEATURE:
                 (D)   OTHER INFORMATION:  OLIGOMER ADR-1


      (xi)       SEQUENCE DESCRIPTION: SEQ ID NO: 49:

GGCTGGGATC TAGGC                                                 15


(2)   INFORMATION FOR SEQ ID NO: 50:
```

(i)   SEQUENCE CHARACTERISTICS:
            (A)   LENGTH: 36 BASE PAIRS
            (B)   TYPE: NUCLEIC ACID
            (C)   STRANDEDNESS: SINGLE
            (D)   TOPOLOGY: LINEAR

(ix)   FEATURE:
            (D)   OTHER INFORMATION: OLIGOMER ADR-2

(xi)   SEQUENCE DESCRIPTION: SEQ ID NO: 50:

CACCACACAG ATCTGGGGGG TCTGCTCCTG TGGGGA   36

(2)   INFORMATION FOR SEQ ID NO: 51:

(i)   SEQUENCE CHARACTERISTICS:
            (A)   LENGTH: 36 BASE PAIRS
            (B)   TYPE: NUCLEIC ACID
            (C)   STRANDEDNESS: SINGLE
            (D)   TOPOLOGY: LINEAR

(ix)   FEATURE:
            (D)   OTHER INFORMATION: OLIGOMER ADR-3

(xi)   SEQUENCE DESCRIPTION: SEQ ID NO: 51:

TTCCATCAGC CGCTTCCTCG GGCGAGCGGC CTCCCT   36

(2)   INFORMATION FOR SEQ ID NO: 52:

(i)   SEQUENCE CHARACTERISTICS:
            (A)   LENGTH: 36
            (B)   TYPE: NUCLEIC ACID
            (C)   STRANDEDNESS: SINGLE
            (D)   TOPOLOGY: LINEAR

(ix)   FEATURE:
            (D)   OTHER INFORMATION: OLIGOMER ADR-4

(xi)   SEQUENCE DESCRIPTION: SEQ ID NO: 52:

CGAGTGTCGA CAAAAATGTC CACACAGGAG CAGACC   36

(2)   INFORMATION FOR SEQ ID NO: 53:

    (i)   SEQUENCE CHARACTERISTICS:
                (A)   LENGTH: 36 BASE PAIRS
                (B)   TYPE: NUCLEIC ACID
                (C)   STRANDEDNESS: SINGLE

                (D)   TOPOLOGY: LINEAR

    (ix)   FEATURE:
                (D)   OTHER INFORMATION: OLIGOMER ADR-5

    (xi)   SEQUENCE DESCRIPTION: SEQ ID NO: 53:

CGTGCTCGAG GTACCTCAGT GCCCCAGCAG CCGCAG   36

(2)   INFORMATION FOR SEQ ID NO: 54:

    (i)   SEQUENCE CHARACTERISTICS:
                (A)   LENGTH: 50 BASE PAIRS
                (B)   TYPE: NUCLEIC ACID
                (C)   STRANDEDNESS: SINGLE
                (D)   TOPOLOGY: LINEAR

    (ix)   FEATURE:
                (D)   OTHER INFORMATION: SYNTHETIC OLIGOMER
                       USED TO SCREEN BOVINE ADRENAL CORTEX
                       cDNA LIBRARY

    (xi)   SEQUENCE DESCRIPTION: SEQ ID NO: 54:

TGCCAGTTCG TAGAGCACAT TGGTGCGTGG CGGGTTAGTG   40

ATGTCCAGGT   50

(2)   INFORMATION FOR SEQ ID NO: 55:

    (i)   SEQUENCE CHARACTERISTICS:
                (A)   LENGTH: 18 BASE PAIRS
                (B)   TYPE: NUCLEIC ACID
                (C)   STRANDEDNESS: DOUBLE

```
                    (D)   TOPOLOGY:  UNKNOWN

        (ix)        FEATURE:
                    (D)   OTHER INFORMATION:  REGION OF ADR cDNA
                          HOMOLOGOUS TO PRIMERS, FIGURE 40

        (xi)        SEQUENCE DESCRIPTION: SEQ ID NO: 55:

CAGCACTTCT CCACACAG                                         18


(2)   INFORMATION FOR SEQ ID NO: 56:

        (i)         SEQUENCE CHARACTERISTICS:
                    (A)   LENGTH:  18 BASE PAIRS
                    (B)   TYPE:  NUCLEIC ACID
                    (C)   STRANDEDNESS:  DOUBLE
                    (D)   TOPOLOGY:  UNKNOWN

        (ix)        FEATURE:
                    (D)   OTHER INFORMATION:  REGION OF ADR cDNA
                          HOMOLOGOUS TO PRIMERS, FIGURE 40

        (xi)        SEQUENCE DESCRIPTION: SEQ ID NO: 56:

GGGCACTGAG CCTAGATC                                         18


(2)   INFORMATION FOR SEQ ID NO: 57:

        (i)         SEQUENCE CHARACTERISTICS:
                    (A)   LENGTH:  27 BASE PAIRS
                    (B)   TYPE:  NUCLEIC ACID
                    (C)   STRANDEDNESS:  SINGLE
                    (D)   TOPOLOGY:  LINEAR

        (ix)        FEATURE:
                    (D)   OTHER INFORMATION:  PRIMER ADR4,
                          FIGURE 40

        (xi)        SEQUENCE DESCRIPTION: SEQ ID NO: 57:

CGAGTGTCGA CAAAAATGTC CACACAG                               27
```

(2)   INFORMATION FOR SEQ ID NO: 58:

    (i)   ·   SEQUENCE CHARACTERISTICS:
        (A)   LENGTH: 24 BASE PAIRS
        (B)   TYPE: NUCLEIC ACID
        (C)   STRANDEDNESS: SINGLE
        (D)   TOPOLOGY: LINEAR

    (ix)   FEATURE:
        (D)   OTHER INFORMATION: PRIMER ADR5,
            FIGURE 40

    (xi)   SEQUENCE DESCRIPTION: SEQ ID NO: 58:

GGGCACTGAG GTACCTCGAG CACG   24

(2)   INFORMATION FOR SEQ ID NO: 59:

    (i)   SEQUENCE CHARACTERISTICS:
        (A)   LENGTH: 25 BASE PAIRS
        (B)   TYPE: NUCLEIC ACID
        (C)   STRANDEDNESS: SINGLE
        (D)   TOPOLOGY: LINEAR

    (xi)   SEQUENCE DESCRIPTION: SEQ ID NO: 59:

GCGCTCAGCG GCCGCTTTCC AGTCG   25

(2)   INFORMATION FOR SEQ ID NO: 60:

    (i)   SEQUENCE CHARACTERISTICS:
        (A)   LENGTH: 21 BASE PAIRS
        (B)   TYPE: NUCLEIC ACID
        (C)   STRANDEDNESS: SINGLE
        (D)   TOPOLOGY: LINEAR

    (xi)   SEQUENCE DESCRIPTION: SEQ ID NO: 60:

AATTGCGGCC GCGTACGTAT G   21

(2)   INFORMATION FOR SEQ ID NO: 61:

(i)   SEQUENCE CHARACTERISTICS:
        (A)   LENGTH: 21 BASE PAIRS
        (B)   TYPE: NUCLEIC ACID
        (C)   STRANDEDNESS: SINGLE
        (D)   TOPOLOGY: LINEAR

(xi)   SEQUENCE DESCRIPTION: SEQ ID NO: 61:

AATTCATACG TACGCGGCCG C   21

(2)   INFORMATION FOR SEQ ID NO: 62:

        (i)   SEQUENCE CHARACTERISTICS:
                (A)   LENGTH: 55 BASE PAIRS
                (B)   TYPE: NUCLEIC ACID
                (C)   STRANDEDNESS: SINGLE
                (D)   TOPOLOGY: LINEAR

        (xi)   SEQUENCE DESCRIPTION: SEQ ID NO: 62:

GAATTCATAC GTACGCGGCC GCAATTGCGG CCGGTACGTA   40

TAATTCACTG GCCGT   55

(2)   INFORMATION FOR SEQ ID NO: 63:

        (i)   SEQUENCE CHARACTERISTICS:
                (A)   LENGTH: 14 BASE PAIRS
                (B)   TYPE: NUCLEIC ACID
                (C)   STRANDEDNESS: SINGLE
                (D)   TOPOLOGY: LINEAR

        (xi)   SEQUENCE DESCRIPTION: SEQ ID NO: 63:

CAACGCGTCC TAGG   14

(2)   INFORMATION FOR SEQ ID NO: 64:

        (i)   SEQUENCE CHARACTERISTICS:
                (A)   LENGTH: 22 BASE PAIRS
                (B)   TYPE: NUCLEIC ACID

(C) STRANDEDNESS: SINGLE
(D) TOPOLOGY: LINEAR

(xi)   SEQUENCE DESCRIPTION: SEQ ID NO: 64:

AATTCCTAGG ACGCGTTGAG CT   22

(2) INFORMATION FOR SEQ ID NO: 65:

(i)   SEQUENCE CHARACTERISTICS:
(A) LENGTH: 33 BASE PAIRS
(B) TYPE: NUCLEIC ACID
(C) STRANDEDNESS: SINGLE
(D) TOPOLOGY: LINEAR

(xi)   SEQUENCE DESCRIPTION: SEQ ID NO: 65:

GATCCGCAGA TATCATCTAG ATCCCGGGTA GAT   33

(2) INFORMATION FOR SEQ ID NO: 66:

(i)   SEQUENCE CHARACTERISTICS:
(A) LENGTH: 39 BASE PAIRS
(B) TYPE: NUCLEIC ACID
(C) STRANDEDNESS: SINGLE
(D) TOPOLOGY: LINEAR

(xi)   SEQUENCE DESCRIPTION: SEQ ID NO: 66:

AGAGCTCAAG ATCTACCCGG GATCTAGATG ATATCTGCG   39

(2) INFORMATION FOR SEQ ID NO: 67:

(i)   SEQUENCE CHARACTERISTICS:
(A) LENGTH: 34 BASE PAIRS
(B) TYPE: NUCLEIC ACID
(C) STRANDEDNESS: SINGLE
(D) TOPOLOGY: LINEAR

(xi)   SEQUENCE DESCRIPTION: SEQ ID NO: 67:

CTTGAGCTCT ACGCAGCTGG TCGACACCTA GGAG   34

(2)   INFORMATION FOR SEQ ID NO: 68:

    (i)   SEQUENCE CHARACTERISTICS:
           (A)   LENGTH: 28 BASE PAIRS
           (B)   TYPE: NUCLEIC ACID
           (C)   STRANDEDNESS: SINGLE
           (D)   TOPOLOGY: LINEAR

    (xi)   SEQUENCE DESCRIPTION: SEQ ID NO: 68:

AATTCTCCTA GGTGTCGACC AGCTGCGT   28

(2)   INFORMATION FOR SEQ ID NO: 69:

    (i)   SEQUENCE CHARACTERISTICS:
           (A)   LENGTH: 40 BASE PAIRS
           (B)   TYPE: NUCLEIC ACID
           (C)   STRANDEDNESS: SINGLE
           (D)   TOPOLOGY: LINEAR

    (xi)   SEQUENCE DESCRIPTION: SEQ ID NO: 69:

GCGGATCTGC TCGAAGATTG CCTGCGCGTT GGGCTTGATC   40

(2)   INFORMATION FOR SEQ ID NO: 70:

    (i)   SEQUENCE CHARACTERISTICS:
           (A)   LENGTH: 15 BASE PAIRS
           (B)   TYPE: NUCLEIC ACID
           (C)   STRANDEDNESS: SINGLE
           (D)   TOPOLOGY: LINEAR

    (xi)   SEQUENCE DESCRIPTION: SEQ ID NO: 70:

TCGACGGACG CGTGG   15

(2)   INFORMATION FOR SEQ ID NO: 71:

    (i)   SEQUENCE CHARACTERISTICS:
           (A)   LENGTH: 14 BASE PAIRS

          (B)   TYPE: NUCLEIC ACID
          (C)   STRANDEDNESS: SINGLE
          (D)   TOPOLOGY: LINEAR

     (xi)   SEQUENCE DESCRIPTION: SEQ ID NO: 71:

TCGACCACGC GTCC   14

(2) INFORMATION FOR SEQ ID NO: 72:

     (i)   SEQUENCE CHARACTERISTICS:
          (A)   LENGTH: 35 BASE PAIRS
          (B)   TYPE: NUCLEIC ACID
          (C)   STRANDEDNESS: SINGLE
          (D)   TOPOLOGY: LINEAR

     (xi)   SEQUENCE DESCRIPTION: SEQ ID NO: 72:

TGGCCGTCGT TTTACTCCTG CGCCTGATGC GGTAT   35

(2) INFORMATION FOR SEQ ID NO: 73:

     (i)   SEQUENCE CHARACTERISTICS:
          (A)   LENGTH: 15 BASE PAIRS
          (B)   TYPE: NUCLEIC ACID
          (C)   STRANDEDNESS: SINGLE
          (D)   TOPOLOGY: LINEAR

     (xi)   SEQUENCE DESCRIPTION: SEQ ID NO: 73:

GGCCGCAAAA CCAAA   15

(2) INFORMATION FOR SEQ ID NO: 74:

     (i)   SEQUENCE CHARACTERISTICS:
          (A)   LENGTH: 15 BASE PAIRS
          (B)   TYPE: NUCLEIC ACID
          (C)   STRANDEDNESS: SINGLE
          (D)   TOPOLOGY: LINEAR

     (xi)   SEQUENCE DESCRIPTION: SEQ ID NO: 74:

AGCTTTTGGT TTTGC   15

(2)   INFORMATION FOR SEQ ID NO: 75:

       (i)   SEQUENCE CHARACTERISTICS:
                   (A)   LENGTH: 20 BASE PAIRS
                   (B)   TYPE: NUCLEIC ACID
                   (C)   STRANDEDNESS: SINGLE
                   (D)   TOPOLOGY: LINEAR

       (xi)   SEQUENCE DESCRIPTION: SEQ ID NO: 75:

GATCTATCGA TGCGGCCGCG   20

(2)   INFORMATION FOR SEQ ID NO: 76:

       (i)   SEQUENCE CHARACTERISTICS:
                   (A)   LENGTH: 20 BASE PAIRS
                   (B)   TYPE: NUCLEIC ACID
                   (C)   STRANDEDNESS: SINGLE
                   (D)   TOPOLOGY: LINEAR

       (xi)   SEQUENCE DESCRIPTION: SEQ ID NO: 76:

CGCGCGCGGC CGCATCGATA   20

(2)   INFORMATION FOR SEQ ID NO: 77:

       (i)   SEQUENCE CHARACTERISTICS:
                   (A)   LENGTH: 14 BASE PAIRS
                   (B)   TYPE: NUCLEIC ACID
                   (C)   STRANDEDNESS: SINGLE
                   (D)   TOPOLOGY: LINEAR

       (xi)   SEQUENCE DESCRIPTION: SEQ ID NO: 77:

AATTGGACGC GTCC   14

(2)   INFORMATION FOR SEQ ID NO: 78:

422161_1

(i)   SEQUENCE CHARACTERISTICS:
           (A)   LENGTH: 12 BASE PAIRS
           (B)   TYPE: NUCLEIC ACID
           (C)   STRANDEDNESS: SINGLE
           (D)   TOPOLOGY: LINEAR

(xi)   SEQUENCE DESCRIPTION: SEQ ID NO: 78:

CACAAGCTTG TG   12

(2)   INFORMATION FOR SEQ ID NO: 79:

(i)   SEQUENCE CHARACTERISTICS:
           (A)   LENGTH: 12 BASE PAIRS
           (B)   TYPE: NUCLEIC ACID
           (C)   STRANDEDNESS: SINGLE
           (D)   TOPOLOGY: LINEAR

(xi)   SEQUENCE DESCRIPTION: SEQ ID NO: 79:

TCGAGGGAAG CT   12